

Das erat- SEQ 10 10-1

RESULT 4

US-10-275-998-10

; Sequence 10, Application US/10275998

; Publication No. US20040023354A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: DAS, Debopriya

; APPLICANT: REDDY, Roopa

; APPLICANT: YAO, Monique G.

; APPLICANT: NGUYEN, Danniell B.

; APPLICANT: LU, Yan

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: YUE, Henry

; APPLICANT: KHAN, Farrah A.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: AU-YOUNG, Janice

; APPLICANT: LAL, Preeti

; APPLICANT: KEARNEY, Liam

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: DING, Li

; APPLICANT: THORNTON, Michael

; TITLE OF INVENTION: LIPID METABOLISM ENZYMES

; FILE REFERENCE: PI-0095 USN

; CURRENT APPLICATION NUMBER: US/10/275,998

; CURRENT FILING DATE: 2002-11-08

; PRIOR APPLICATION NUMBER: US 01/15210

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/203,511

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: US 60/207,903

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: US 60/210,150

; PRIOR FILING DATE: 2000-06-07

; PRIOR APPLICATION NUMBER: US 60/213,392

; PRIOR FILING DATE: 2000-06-23

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PERL Program

; SEQ ID NO 10

; LENGTH: 4237

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20040023354A1 7472768CB1

US-10-275-998-10

Query Match 79.5%; Score 3684.6; DB 8; Length 4237;

Best Local Similarity 94.6%; Pred. No. 0;

Matches 3926; Conservative 0; Mismatches 4; Indels 219; Gaps 2;

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Qy      546 GTGGAGCGGTGCATGGGTGCCATGCAAGAGGGGATGCAGATGGTGAAGCTGCGTGGCGGC 605
          |||
Db      87  GTGGAGCGGTGCATGGGTGCCATGCAAGAGGGGATGCAGATGGTGAAGCTGCGTGGCGGC 146

Qy      606 TCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG 665
          |||
Db      147 TCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG 206

Qy      666 CCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTGAGTGAG 725
          |||
Db      207 CCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTGAGTGAG 266

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Qy	726	GGGCGGCAGTCGGAGGTCTTCCAGCGCTACCCTGACGGCAGCTTCGACCCCAACTGCTGC	785
Db	267	GGGCGGCAGTCGGAGGTCTTCCAGCGCTACCCTGACGGCAGCTTCGACCCCAACTGCTGC	326
Qy	786	TTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	845
Db	327	TTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	386
Qy	846	GTGGCGCGCACCTGGGTCACTGGCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	905
Db	387	GTGGCGCGCACCTGGGTCACTGGCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	446
Qy	906	AGCCTGGCTCGCCGCCAGCGCACCAGGGACC-----	936
Db	447	AGCCTGGCTCGCCGCCAGCGCACCAGGGACCAATATCCTTGGGCACCTATCGGGCAATGC	506
Qy	937	-----	936
Db	507	AGACCCAGGGACCGGCCCTTGGCTGCTCACCTGGGGGGCCTGTCTTTGCCGGGTCA	566
Qy	937	-----AGTGGCTGAAGCAGACGTTTGACGAGGCC	965
Db	567	CACACTGGGGAAGTGGCCGGCCAGAGGGTGAGTGGCTGAAGCAGACGTTTGACGAGGCC	626
Qy	966	GACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTGCAGCTGCTGCACAAGCTC	1025
Db	627	GACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTGCAGCTGCTGCACAAGCTC	686
Qy	1026	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTT CAG-----	1066
Db	687	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTT CAGGGTGGCTGGTCATGCCTGG	746
Qy	1067	-----	1066
Db	747	CTGGAGCAAGGGAAGCTGGCCTGCTCACAGGACAGGGCCCTGGTTCGAGGTGCCAATGGGG	806
Qy	1067	-----GGAAGCGGACACGGATGACCACCAAGGGACGCTGGGTTTT	1106
Db	807	ACCCAAGGCCTTGCAATTGCAGGAAGCGGACACGGATGACCACCAAGGGACGCTGGGTTTT	866
Qy	1107	GAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGCCGGGACCTCTACCTGCTCATG	1166
Db	867	GAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGCCGGGACCTCTACCTGCTCATG	926
Qy	1167	CTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCCAGCCTGCAGCGCTTCCTGCAG	1226
Db	927	CTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCCAGCCTGCAGCGCTTCCTGCAG	986
Qy	1227	GTGGAGCAGAAGATGGCGGGTGTGACCTCGAGAGCTGCCAGGACATCATCGAGCAGTTT	1286
Db	987	GTGGAGCAGAAGATGGCGGGTGTGACCTCGAGAGCTGCCAGGACATCATCGAGCAGTTT	1046
Qy	1287	GAGCCATGCCCAGAAAAAAGAGTAAGGGGCTGCTGGGCATTGATGGCTTCACCAACTAC	1346
Db	1047	GAGCCATGCCCAGAAAAAAGAGTAAGGGGCTGCTGGGCATTGATGGCTTCACCAACTAC	1106
Qy	1347	ACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCACCACCATGTGCACCAGGACATG	1406
Db	1107	ACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCACCACCATGTGCACCAGGACATG	1166

Qy	14 07	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAACACCTACCTCGTGGGTGAC	14 66
Db	11 67	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAACACCTACCTCGTGGGTGAC	12 26
Qy	14 67	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	15 26
Db	12 27	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	12 86
Qy	15 27	TGCGTGGAGGTGGACTGCTGGGATGGGCCCGACGGGGAGCCCATTGTGCACCATGGCTAC	15 86
Db	12 87	TGCGTGGAGGTGGACTGCTGGGATGGGCCCGACGGGGAGCCCATTGTGCACCATGGCTAC	13 46
Qy	15 87	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAAACCATCAACAAATATGCCTTC	16 46
Db	13 47	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAAACCATCAACAAATATGCCTTC	14 06
Qy	16 47	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	17 06
Db	14 07	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	14 66
Qy	17 07	AAGAAAAATGGCCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	17 66
Db	14 67	AAGAAAAATGGCCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	15 26
Qy	17 67	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	18 26
Db	15 27	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	15 86
Qy	18 27	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	18 86
Db	15 87	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	16 46
Qy	18 87	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	19 46
Db	16 47	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	17 06
Qy	19 47	AATCGAAAGCGTGTAAGAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	20 06
Db	17 07	AATCGAAAGCGTGTAAGAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	17 66
Qy	20 07	AAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTCTCCACACTGTCCCATCTGGA	20 66
Db	17 67	AAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTCTCCACACTGTCCCATCTGGA	18 26
Qy	20 67	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	21 26
Db	18 27	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	18 86
Qy	21 27	AGCAGACGCAATGGCCGCTCGTCTGTTGGAAGCTTCTCCAGGCGCAAGAAGAAGGGCAGC	21 86
Db	18 87	AGCAGACGCAATGGCCGCTCGTCTGTTGGAAGCTTCTCCAGGCGCAAGAAGAAGGGCAGC	19 46
Qy	21 87	AAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGAGATGAGGGTCAGGACTCCCCGGGAGGC	22 46
Db	19 47	AAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGAGATGAGGGTCAGGACTCCCCGGGAGGC	20 06
Qy	22 47	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	23 06
Db	20 07	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	20 66
Qy	23 07	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	23 66

Db	2067	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	2126
Qy	2367	TGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACAGATTCTGCAGCAGAAGCCGGCG	2426
Db	2127	TGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACAGATTCTGCAGCAGAAGCCGGCG	2186
Qy	2427	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCGCATCTACCCCTCCTCCTACCGTGTG	2486
Db	2187	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCGCATCTACCCCTCCTCCTACCGTGTG	2246
Qy	2487	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2546
Db	2247	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2306
Qy	2547	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2606
Db	2307	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2366
Qy	2607	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTCAACCCCAACTCG	2666
Db	2367	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTCAACCCCAACTCG	2426
Qy	2667	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2726
Db	2427	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2486
Qy	2727	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTTT	2786
Db	2487	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTTT	2546
Qy	2787	GTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGCAGGGAGCAGACCCGCGTGGTG	2846
Db	2547	GTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGCAGGGAGCAGACCCGCGTGGTG	2606
Qy	2847	GACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2906
Db	2607	GACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2666
Qy	2907	GAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2966
Db	2667	GAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2726
Qy	2967	GGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTAGAA	3026
Db	2727	GGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTGGAG	2786
Qy	3027	GGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTCAGTGACATCAGCGGTAAGGTC	3086
Db	2787	GGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTCAGTGACATCAGCGGTAAGGTC	2846
Qy	3087	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCAAAGCCCGGCTCGCTGGAC	3146
Db	2847	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCAAAGCCCGGCTCGCTGGAC	2906
Qy	3147	AGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	3206
Db	2907	AGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	2966
Qy	3207	ACGGCCAGCGCCCGACCAAGAGCAGAAGCCGGGCCGAGGGGCTTCCCGGAGCTGGTC	3266

Db	2967	ACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGAGGGGCTTCCCGGAGCTGGTC	3026
Qy	3267	CTGGGTACACGGGACACAGGCTCCAAGGGGGTGGCAGACGATGTGGTGCCCCCGGGCCC	3326
Db	3027	CTGGGTACACGGGACACAGGCTCCAAGGGGGTGGCAGACGATGTGGTGCCCCCGGGCCC	3086
Qy	3327	GGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCGGCAGCGGCAGCCCCGAGGTAAG	3386
Db	3087	GGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCGGCAGCGGCAGCCCCGAGGTAAG	3146
Qy	3387	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCGCGTGTCTGGAC	3446
Db	3147	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCGCGTGTCTGGAC	3206
Qy	3447	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3506
Db	3207	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3266
Qy	3507	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCCGGGGCCTGCAAGCAGG	3566
Db	3267	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCCGGGGCCTGCAAGCAGG	3326
Qy	3567	CAGGCAGCCATTCGCCAGCAGCCCCGGGCCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3626
Db	3327	CAGGCAGCCATTCGCCAGCAGCCCCGGGCCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3386
Qy	3627	GGCCTGGACCTCAGCTATCCCGGGGAGAAGCAGAGAGGCCCCAAGGGTCCTGGGGCC	3686
Db	3387	GGCCTGGACCTCAGCTATCCCGGGGAGAAGCAGAGAGGCCCCAAGGGTCCTGGGGCC	3446
Qy	3687	TGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3746
Db	3447	TGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3506
Qy	3747	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCTGCAGGCAACCGGGGGCC	3806
Db	3507	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCTGCAGGCAACCGGGGGCC	3566
Qy	3807	CTGCAGGGAGAGATGAGTGCCCTTGTTTGCTCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3866
Db	3567	CTGCAGGGAGAGATGAGTGCCCTTGTTTGCTCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3626
Qy	3867	CCCATGTTCTCCGCCGGTAAGCCCCTCTTGCCCTGCGTGGTCCTCCCGCACGCCCTGGC	3926
Db	3627	CCCATGTTCTCCGCCGGTAAGCCCCTCTTGCCCTGCGTGGTCCTCCCGCACGCCCTGGC	3686
Qy	3927	ATGGCTGGGCCTGGGTACCTGCTGCTGCTTCTGCGTGGACGGTGTGCCTCGTGTGCTC	3986
Db	3687	ATGGCTGGGCCTGGGTACCTGCTGCTGCTTCTGCGTGGACGGTGTGCCTCGTGTGCTC	3746
Qy	3987	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	4046
Db	3747	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	3806
Qy	4047	TGTGGCCCATAGCCCCAGCCCTCCTGTCTGAGCTTGAGGCCCTGGGACTTGGGTGGAGCT	4106
Db	3807	TGTGGCCCATAGCCCCAGCCCTCCTGTCTGAGCTTGAGGCCCTGGGACTTGGGTGGAGCT	3866
Qy	4107	GGTTTGAGGCCCCGACAGGCTGGGAAGAACCAGCTGCTCTTGCTGAGGGTCTGGGGCCGGG	4166
Db	3867	GGTTTGAGGCCCCGACAGGCTGGGAAGAACCAGCTGCTCTTGCTGAGGGTCTGGGGCCGGG	3926

Qy	4167	ACTGTGGCCTGACATGCTGGGCCCCTCCGGCTGGGCGCTTCCCCAAACTCACCTCCTGGG	4226
Db	3927	ACTGTGGCCTGACATGCTGGGCCCCTCCGGCTGGGCGCTTCCCCAAACTCACCTCCTGGG	3986
Qy	4227	CGGCTGGCGACCTGCATGGCCCCTGATGCCTTTCCTGGGACTGGGGGCCATGTACCATCC	4286
Db	3987	CGGCTGGCGACCTGCATGGCCCCTGATGCCTTTCCTGGGACTGGGGGCCACGTACCATCC	4046
Qy	4287	CATTTCCACCTCCCTCTAGGGCAGGCTCCAGGGGTCCCTACTGGGAAGTCTGATGTGGGC	4346
Db	4047	CATTTCCACCTCCCTCTAGGGCAGGCTCCAGGGGTCCCTACTGGGAAGTCTGATGTGGGC	4106
Qy	4347	AGGTAGTGCAGCTGCTGGGCGTCTCCTGCGCCCCCTGGGACGCCTGGAGCCTGCTGAGTGC	4406
Db	4107	AGGTAGTGCAGCTGCTGGGCGTCTCCTGCGCCCCCTGGGACGCCTGGAGCCTGCTGAGTGC	4166
Qy	4407	TGCGTGGAGTAGATTCCCTGGGCCCCAGGGCTTCGCTGCTTTGGGCTGAAGCACCCACT	4466
Db	4167	TGCGTGGAGTAGATTCCCTGGGCCCCAGGGCTTCGCTGCTTTGGGCTGAAGCACCCACT	4226
Qy	4467	AGAAGGGTG	4475
Db	4227	AGAAGGGTG	4235

Day et al - Seq ID No. 2

RESULT 4

US-10-275-998-5

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; Sequence 5, Application US/10275998
; Publication No. US20040023354A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAS, Debopriya
; APPLICANT: REDDY, Roopa
; APPLICANT: YAO, Monique G.
; APPLICANT: NGUYEN, Danniell B.
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: DING, Li
; APPLICANT: THORNTON, Michael
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0095 USN
; CURRENT APPLICATION NUMBER: US/10/275,998
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 01/15210
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203,511
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/207,903
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/210,150
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/213,392
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023354A1 7472768CD1
US-10-275-998-5
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Query Match 95.5%; Score 6092.5; DB 4; Length 1239;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 1166; Conservative 0; Mismatches 0; Indels 73; Gaps 2;

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Qy      42 MGAMQEGMQMVKL RGGSKGLVRFYYLDEHRSCIRWRPSRKNEKAKISIDSIQEVSEGRQS 101
      |||
Db      1 MGAMQEGMQMVKL RGGSKGLVRFYYLDEHRSCIRWRPSRKNEKAKISIDSIQEVSEGRQS 60

Qy     102 EVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSSEVARTWVTGLRYLMAGISDEDSLAR 161
      |||
Db      61 EVFQRYPDGSFDPNCCFSIYHGSHRESLDLVSTSSEVARTWVTGLRYLMAGISDEDSLAR 120

Qy     162 RQRTRDQ-----WLKQTFDEADKNG 181
      |||
Db     121 RQRTRDQYPWAPIGQCRPRDRPLGCS PWGGLSFAGSHTGEVAGQ RVEWLKQTFDEADKNG 180
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Qy	182	DGSLSIGEVLLHKLNVNLPQRVKQMF-----	211
Db	181	DGSLSIGEVLLHKLNVNLPQRVKQMFVAGHAWLEQGKLACSQDRALVEVPMGTQGL	240
Qy	212	---EADTDDHQGTLGFEFCAFYKMMSTRRDYLLMLTYSNHKDHLDAASLQRFQVEQK	268
Db	241	ALQEADTDDHQGTLGFEFCAFYKMMSTRRDYLLMLTYSNHKDHLDAASLQRFQVEQK	300
Qy	269	MAGVTLESCQDIEQFEPCPENKSKGLLGIDGFTNYTRSPAGDIFNPEHHHVHQDMTQPL	328
Db	301	MAGVTLESCQDIEQFEPCPENKSKGLLGIDGFTNYTRSPAGDIFNPEHHHVHQDMTQPL	360
Qy	329	SHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEPVHHGYTLTS	388
Db	361	SHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWDGPDGEPVHHGYTLTS	420
Qy	389	KILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLTDLGDKLDLSSVSSD	448
Db	421	KILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLTDLGDKLDLSSVSSD	480
Qy	449	ATTLSPQMLKGKILVKGKKLPANISEDAAEEGEVSDSDADEIDDDCKLLNGDASTNRKR	508
Db	481	ATTLSPQMLKGKILVKGKKLPANISEDAAEEGEVSDSDADEIDDDCKLLNGDASTNRKR	540
Qy	509	VENTAKRKLDSLIKESKIRDCEDPNNFSVSTLSPSGKLGRKSKAEEDVESGEDAGASRRN	568
Db	541	VENTAKRKLDSLIKESKIRDCEDPNNFSVSTLSPSGKLGRKSKAEEDVESGEDAGASRRN	600
Qy	569	GRLVVGFSFRRKKKGSKLKAASVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLVKY	628
Db	601	GRLVVGFSFRRKKKGSKLKAASVEEGDEGQDSPGGQSRGATRQKKTMKLSRALSDLVKY	660
Qy	629	TKSVATHDIEMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQQQLSRIYPSSYRVDSSN	688
Db	661	TKSVATHDIEMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQQQLSRIYPSSYRVDSSN	720
Qy	689	YNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSEDPL	748
Db	721	YNPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSEDPL	780
Qy	749	PGQLKKQLVLRISGQQLPKPRDSMLGDRGEIIDPFVEVEIIGLPVDCSREQTRVDDNG	808
Db	781	PGQLKKQLVLRISGQQLPKPRDSMLGDRGEIIDPFVEVEIIGLPVDCSREQTRVDDNG	840
Qy	809	FNPTWEETLVFMVHMPEIALVRFLVWDHDPIGRDFIGQRTLAFSSMMPGYRHVYLEGMEE	868
Db	841	FNPTWEETLVFMVHMPEIALVRFLVWDHDPIGRDFIGQRTLAFSSMMPGYRHVYLEGMEE	900
Qy	869	ASIFVHVAVSDISGKVKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASA	928
Db	901	ASIFVHVAVSDISGKVKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASA	960
Qy	929	PTKSQKPGRRGFPELVLTGTRDTGSKGVADDVPPGPGPAPEAPAEQEGPGSGSPRGKAPAA	988
Db	961	PTKSQKPGRRGFPELVLTGTRDTGSKGVADDVPPGPGPAPEAPAEQEGPGSGSPRGKAPAA	1020
Qy	989	VAEKSPVRVRPVRVLDGPGPAGMAATCMKCVVGSAGVNTGGLQRRERPPSPGPASRQAAI	1048
Db	1021	VAEKSPVRVRPVRVLDGPGPAGMAATCMKCVVGSAGVNTGGLQRRERPPSPGPASRQAAI	1080

Qy	1049	RQQPRARADSLGAPCCGLDPHAIPGRSREAPKGP	QAWRQGP	GGSGSMSSDSSSPDSPGIP	1108
Db	1081	RQQPRARADSLGAPCCGLDPHAIPGRSREAPKGP	QAWRQGP	GGSGSMSSDSSSPDSPGIP	1140
Qy	1109	ERSPRWPEGACRQPGALQGEMSALFAQLEEIRSKSPMFSAGKPLLPCVVLP	HAPGMAGP	1168	
Db	1141	ERSPRWPEGACRQPGALQGEMSALFAQLEEIRSKSPMFSAGKPLLPCVVLP	HAPGMAGP	1200	
Qy	1169	GSPAAASAWTVSPRVLVLVALYPWHCLRG	TLLPWLACGP	1207	
Db	1201	GSPAAASAWTVSPRVLVLVALYPWHCLRG	TLLPWLACGP	1239	

Qy	292	GGGCGGCAGTCGGAGGTCTTCCAGCGCTACCCCTGACGGCAGCTTCGACCCCAACTGCTGC	351
Db	267	GGGCGGCAGTCGGAGGTCTTCCAGCGCTACCCCTGACGGCAGCTTCGACCCCAACTGCTGC	326
Qy	352	TTCAGCATCTACCACGGCAGCCACCGCAGTCTGCTGGACCTGGTCTCCACCAGCAGCGAG	411
Db	327	TTCAGCATCTACCACGGCAGCCACCGCAGTCTGCTGGACCTGGTCTCCACCAGCAGCGAG	386
Qy	412	GTGGCGCGCACCTGGGTCACTGGCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	471
Db	387	GTGGCGCGCACCTGGGTCACTGGCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	446
Qy	472	AGCCTGGCTCGCCGCCAGCGCACCAGGGACC-----	502
Db	447	AGCCTGGCTCGCCGCCAGCGCACCAGGGACCAATATCCTTGGGCACCTATCGGGCAATGC	506
Qy	503	-----	502
Db	507	AGACCCAGGGACCGGCCCTTGGCTGCTCACCTTGGGGGGCCTGTCTTTGCCGGGTCA	566
Qy	503	-----AGTGGCTGAAGCAGACGTTTGACGAGGCC	531
Db	567	CACACTGGGGAAGTGCCCGGCCAGAGGTGGAGTGGCTGAAGCAGACGTTTGACGAGGCC	626
Qy	532	GACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTGCAGCTGCTGCACAAGCTC	591
Db	627	GACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTGCAGCTGCTGCACAAGCTC	686
Qy	592	AACGTGAACCTGCCCCGGCAGAGGTGAAGCAGATGTT CAG-----	632
Db	687	AACGTGAACCTGCCCCGGCAGAGGTGAAGCAGATGTT CAGGGTGGCTGGTCATGCCTGG	746
Qy	633	-----	632
Db	747	CTGGAGCAAGGGAAGCTGGCCTGCTCACAGGACAGGGCCCTGGTCGAGGTGCCAATGGGG	806
Qy	633	-----GGAAGCGGACACGGATGACCACCAAGGGACGCTGGGTTTT	672
Db	807	ACCCAAGGCCTTGCAATTGCAGGAAGCGGACACGGATGACCACCAAGGGACGCTGGGTTTT	866
Qy	673	GAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGCCGGGACCTCTACCTGCTCATG	732
Db	867	GAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGCCGGGACCTCTACCTGCTCATG	926
Qy	733	CTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCCAGCCTGCAGCGCTTCCTGCAG	792
Db	927	CTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCCAGCCTGCAGCGCTTCCTGCAG	986
Qy	793	GTGGAGCAGAAGATGGCGGGTGTGACCTCGAGAGCTGCCAGGACATCATCGAGCAGTTT	852
Db	987	GTGGAGCAGAAGATGGCGGGTGTGACCTCGAGAGCTGCCAGGACATCATCGAGCAGTTT	1046
Qy	853	GAGCCATGCCCAGAAAAAAGAGTAAGGGGCTGCTGGGCATTGATGGCTTCACCAACTAC	912
Db	1047	GAGCCATGCCCAGAAAAAAGAGTAAGGGGCTGCTGGGCATTGATGGCTTCACCAACTAC	1106
Qy	913	ACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCACCACCATGTGCACCAGGACATG	972
Db	1107	ACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCACCACCATGTGCACCAGGACATG	1166

Qy	973	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCACAACACCTACCTCGTGGGTGAC	1032
Db	1167	ACGCAGCCGCTGAGCCACTACTTCATCACCTCGTCCCACAACACCTACCTCGTGGGTGAC	1226
Qy	1033	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	1092
Db	1227	CAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGGGTCCTGCAGGCTGGCTGCCGC	1286
Qy	1093	TGCGTGGAGGTGGACTGCTGGGATGGGCCCGACGGGGAGCCCATGTGTCACCATGGCTAC	1152
Db	1287	TGCGTGGAGGTGGACTGCTGGGATGGGCCCGACGGGGAGCCCATGTGTCACCATGGCTAC	1346
Qy	1153	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAAACCATCAACAAATATGCCTTC	1212
Db	1347	ACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAAACCATCAACAAATATGCCTTC	1406
Qy	1213	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	1272
Db	1407	ATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAACCACTGCAGTGTATCCAGCAG	1466
Qy	1273	AAGAAAAATGGCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	1332
Db	1467	AAGAAAAATGGCCAGTATCTGACTGACATCCTTGGGGACAAGCTGGACCTGTATCAGTG	1526
Qy	1333	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	1392
Db	1527	AGCAGTGAAGATGCCACCACACTCCCTCTCCACAGATGCTCAAGGGCAAGATCCTCGTG	1586
Qy	1393	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	1452
Db	1587	AAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCGGAGGAAGGCGAGGTGTCTGAT	1646
Qy	1453	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	1512
Db	1647	GAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTCCTCAATGGGGATGCATCCACC	1706
Qy	1513	AATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	1572
Db	1707	AATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAACTGGATTCCCTCATCAAAGAGTCG	1766
Qy	1573	AAGATTCGGGACTGTGAGGACCCCAACAATTCTCCGTCTCCACACTGTCCCATCTGGA	1632
Db	1767	AAGATTCGGGACTGTGAGGACCCCAACAATTCTCCGTCTCCACACTGTCCCATCTGGA	1826
Qy	1633	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	1692
Db	1827	AAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAGTCTGGGGAGGATGCCGGGGCC	1886
Qy	1693	AGCAGACGCAATGGCCGCCTCGTCGTGGGAAGCTTCTCCAGGCGCAAGAAGAAGGGCAGC	1752
Db	1887	AGCAGACGCAATGGCCGCCTCGTCGTGGGAAGCTTCTCCAGGCGCAAGAAGAAGGGCAGC	1946
Qy	1753	AAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGAGATGAGGGTCAGGACTCCCGGGAGGC	1812
Db	1947	AAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGAGATGAGGGTCAGGACTCCCGGGAGGC	2006
Qy	1813	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	1872
Db	2007	CAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAGCTGTCCCGGGCCCTCTCTGAC	2066
Qy	1873	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	1932

Db	2067	CTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATAGAGATGGAGGCGGCGTCCAGC	2126
Qy	1933	TGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACCAGATTCTGCAGCAGAAGCCGGCG	1992
Db	2127	TGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACCAGATTCTGCAGCAGAAGCCGGCG	2186
Qy	1993	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCGCATCTACCCCTCCTCCTACCGTGTG	2052
Db	2187	CAGTACCTACGCTTCAACCAGCAGCAGCTCTCCGCATCTACCCCTCCTCCTACCGTGTG	2246
Qy	2053	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2112
Db	2247	GACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCCGGCTGCCAAATGGTTGCCCTG	2306
Qy	2113	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2172
Db	2307	AACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGAGCCAAGTTCAGCGCCAACGGT	2366
Qy	2173	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTCACCCCAACTCG	2232
Db	2367	GGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAGGGCGTGTTCACCCCAACTCG	2426
Qy	2233	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2292
Db	2427	GAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTGCTCCGGATCATCAGTGGCCAG	2486
Qy	2293	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTTT	2352
Db	2487	CAGCTTCCCAAGCCGCGCGACTCCATGCTGGGGGACCGTGGGGAGATCATCGACCCCTTT	2546
Qy	2353	GTGGAGGTGAGATCATTGGGCTCCCTGTGGAAGTGCAGCAGGGAGCAGACCCGCGTGGTG	2412
Db	2547	GTGGAGGTGAGATCATTGGGCTCCCTGTGGAAGTGCAGCAGGGAGCAGACCCGCGTGGTG	2606
Qy	2413	GACGACAACGGGTTCACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2472
Db	2607	GACGACAACGGGTTCACCCACCTGGGAGGAGACCCTGGTTTTCATGGTGCACATGCCG	2666
Qy	2473	GAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2532
Db	2667	GAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGATCCCATCGGGCGTGACTTCATT	2726
Qy	2533	GGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTAGAA	2592
Db	2727	GGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGCTACAGACACGTGTACCTGGAG	2786
Qy	2593	GGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTCACTGACATCAGCGGTAAGGTC	2652
Db	2787	GGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTCACTGACATCAGCGGTAAGGTC	2846
Qy	2653	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCCAAAGCCCGGCTCGCTGGAC	2712
Db	2847	AAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGCCCAAAGCCCGGCTCGCTGGAC	2906
Qy	2713	AGTCATGCTGCTGGGCGGCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	2772
Db	2907	AGTCATGCTGCTGGGCGGCCCGGCCCGGCCCTCCGTTAGCCAGCGGATCCTGCGGCGC	2966
Qy	2773	ACGGCCAGCGCCCGACCAAGAGCCAGAAGCCGGGCCGAGGGCTTCCCGGAGCTGGTC	2832

Db	2967	ACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGAGGGGCTTCCCGAGCTGGTC	3026
Qy	2833	CTGGGTACACGGGACACAGGCTCCAAGGGGGTGGCAGACGATGTGGTGCCCCCGGGCCC	2892
Db	3027	CTGGGTACACGGGACACAGGCTCCAAGGGGGTGGCAGACGATGTGGTGCCCCCGGGCCC	3086
Qy	2893	GGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCCGGCAGCGGCAGCCCCGAGGTAAG	2952
Db	3087	GGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCCGGCAGCGGCAGCCCCGAGGTAAG	3146
Qy	2953	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCCCGCGTGTCTGGAC	3012
Db	3147	GCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTGCGGCCCCCGCGTGTCTGGAC	3206
Qy	3013	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3072
Db	3207	GGCCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAGTGTGTGGTGGGATCCTGCGCC	3266
Qy	3073	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCCGGGGCCTGCAAGCAGG	3132
Db	3267	GGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCCAGCCCCGGGGCCTGCAAGCAGG	3326
Qy	3133	CAGGCAGCCATTCGCCAGCAGCCCCGGGGCCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3192
Db	3327	CAGGCAGCCATTCGCCAGCAGCCCCGGGGCCCGGGCTGACTCACTGGGGGCCCCCTGCTGT	3386
Qy	3193	GGCCTGGACCCTCACGCTATCCCGGGGAGAAGCAGAGAGGCCCCAAGGGTCCTGGGGCC	3252
Db	3387	GGCCTGGACCCTCACGCTATCCCGGGGAGAAGCAGAGAGGCCCCAAGGGTCCTGGGGCC	3446
Qy	3253	TGGAGGCAGGGTCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3312
Db	3447	TGGAGGCAGGGTCAGGCGGTAGCGGCTCCATGTCTCGGACTCCAGCAGCCAGACAGC	3506
Qy	3313	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCTGCAGGCAACCGGGGGCC	3372
Db	3507	CCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGTGCTGCAGGCAACCGGGGGCC	3566
Qy	3373	CTGCAGGGAGAGATGAGTGCCTTGTTTGCTCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3432
Db	3567	CTGCAGGGAGAGATGAGTGCCTTGTTTGCCAAAAGCTGGAGGAGATCAGGAGTAAATCC	3626
Qy	3433	CCCATGTTCTCCGCCGGTAAGCCCCCTCTTGCCCTGCGTGGTCCTCCCGCACGCCCCCTGGC	3492
Db	3627	CCCATGTTCTCCGCCGGTAAGCCCCCTCTTGCCCTGCGTGGTCCTCCCGCACGCCCCCTGGC	3686
Qy	3493	ATGGCTGGGCCTGGGTCACCTGCTGCTGCTTCTGCGTGGACGGTGTGCGCTCGTGTGCTC	3552
Db	3687	ATGGCTGGGCCTGGGTCACCTGCTGCTGCTTCTGCGTGGACGGTGTGCGCTCGTGTGCTC	3746
Qy	3553	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	3612
Db	3747	GTGCTCGTGGCTCTGTATCCGTGGCACTGTCTCCGTGGCACTCTGCTCCCTTGGCTTGCC	3806
Qy	3613	TGTGGCCCATAG	3624
Db	3807	TGTGGCCCATAG	3818